Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

Claims 1-8. (Canceled)

9. (Currently amended) A method for identifying an agent that interacts with an active site of Beta-site APP Cleaving Enzyme (BACE), the method comprising ~~the steps of~~:

~~(a) determining~~ identifying an active site of BACE from a three dimensional model of BACE using the relative structural coordinates of ~~Figure 1~~ BACE as represented in Figures 1A-1EEE, ± a root mean square deviation from the backbone atoms of ~~said amino acids~~ BACE of not more than 1.5 Å; ~~and~~

~~(b)~~ performing computer fitting analysis to identify an agent which interacts with said active site; and

~~(c)~~ obtaining the agent.

10. (Currently Amended) The method of Claim 9, wherein the ± a root mean square deviation from the backbone atoms of ~~said amino acids~~ BACE is not more than 1.0 Å.

11. (Currently Amended) The method of Claim 9, wherein the ± a root mean square deviation from the backbone atoms of ~~said amino acids~~ BACE is not more than 0.5 Å.

12. (Currently amended) A method for identifying an agent that interacts with an active site of ~~an~~ a beta-amyloid precursor protein (APP) binding protein or peptide, the method comprising ~~the steps of~~:

~~(a)~~ generating a three dimensional model of an active site of an APP binding protein or peptide using the relative structural coordinates according to ~~Figure 1~~ Figures 1A-1EEE of

~~residues~~ amino acids SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALAI88, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å; ~~and~~

~~(b)~~ ~~designing~~ identifying an agent using the three dimensional model ~~generated in step (a)~~; and

obtaining the agent.

13. (Original) The method of Claim 12, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

14. (Original) The method of Claim 12, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

15. (Currently amended) The method of Claim 12, wherein the agent is ~~designed~~ identified by performing computer fitting analysis of the agent with the three dimensional model ~~generated in step (a)~~.

16. (Currently amended) The method of Claim 12, further comprising ~~the steps of: (c) obtaining or synthesizing the agent so designed; and (d)~~ contacting the agent with the APP binding protein or peptide in order to determine the effect the agent has on the APP binding protein or peptide.

17. (Original) The method of Claim 12, wherein the APP binding protein or peptide is BACE.

18. (Original) The method of Claim 17, wherein the agent is a potential inhibitor of binding between BACE and APP.

19. (Currently amended) The method of Claim 18, further comprising ~~the steps of: (c) obtaining or synthesizing the agent so designed; and (d)~~ contacting the agent with BACE in the presence of APP.

20. (Currently amended) A method for identifying an agent that interacts with an active site of ~~an~~ a beta-amyloid precursor protein (APP) binding protein or peptide, the method comprising ~~the steps of~~:

~~(a)~~ generating a three dimensional model of an active site of an APP binding protein or peptide using the relative structural coordinates according to ~~Figure 1~~ Figures 1A-1EEE of ~~residues~~ amino acids LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYRI29, VAL130, PRO131, TYR132, THR133, GLN134, GLYI35, LYSI36, TRP137, LYS168, PHE169, PHE170, ILE171, ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALAI83, TYR184, ALAI85, GLU186, ILE187, ALAI88, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAI.370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396 and ILE447, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å; ~~and~~

~~(b) designing~~ identifying an agent using the three dimensional model ~~generated in step (a)~~; and

obtaining the agent.

21. (Original) The method of Claim 18, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

22. (Original) The method of Claim 20, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

23. (Currently amended) The method of Claim 20, wherein the agent is ~~designed~~ identified by performing computer fitting analysis of the agent with the three dimensional model ~~generated in step (a)~~.

24. (Currently amended) The method of Claim 20, further comprising ~~the steps of: (c) obtaining or synthesizing the agent so designed; and (d)~~ contacting the agent with the APP binding protein or peptide in order to determine the effect the agent has on the APP binding protein or peptide.

25. (Original) The method of Claim 20, wherein the APP binding protein or peptide is BACE.

26. (Original) The method of Claim 25, wherein the agent is a potential inhibitor of binding between BACE and APP.

27. (Currently amended) The method of Claim 26, further comprising ~~the steps of: (c) obtaining or synthesizing the agent so designed; and (d)~~ contacting the agent with BACE in the presence of APP.

Claims 28-30. (Canceled)

31. (New) The method of claim 9, wherein the active site of BACE comprises the relative structural coordinates according to ~~Figure 1~~ Figures 1A-1EEE of ~~residues~~ amino acids SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133,

GLN134, ILE171, ILE179, ILE187, ALAl88, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å

32. (New) The method of claim 9, wherein obtaining the agent comprises synthesizing the agent.

33. (New) The method of claim 12, wherein obtaining the agent comprises synthesizing the agent.

34. (New) The method of claim 20, wherein obtaining the agent comprises synthesizing the agent.